

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:40 ; Search time 2351.15 Seconds

(Without alignments)
161.383 Million cell updates/sec

Title: US-09-851-670-14

Perfect score: 23

Sequence: 1 gagacacccgcctctcgcgaac 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Database :

GenEmbl:*

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34: em_hgtg_inv:*
35: em_hgtg_rnd:*
36: em_hgtg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-----------|--------------------|
| 1 | 14.2 | 61.7 | 51 | 6 | AX159518 | AX159518 Sequence |
| 2 | 13.2 | 57.4 | 30 | 6 | AR026622 | AR026622 Sequence |
| 3 | 13.2 | 57.4 | 36 | 9 | S59766 | S59766 IGVH-pre-B- |
| 4 | 13 | 56.5 | 34 | 6 | AX007196 | AX007196 Sequence |
| 5 | 13 | 56.5 | 34 | 6 | AX007368 | AX007368 Sequence |
| 6 | 13 | 56.5 | 51 | 6 | AX160002 | AX160002 Sequence |
| 7 | 13 | 56.5 | 52 | 7 | PQBMS5E | M5754 Bacterioph |
| 8 | 13 | 56.5 | 52 | 7 | PQBMS5E | M25462 Bacterioph |
| 9 | 12.8 | 55.7 | 41 | 6 | A93667 | A93667 Sequence 3 |
| 10 | 12.8 | 55.7 | 50 | 6 | AX158612 | AX158612 Sequence |
| 11 | 12.8 | 55.7 | 51 | 6 | AX159517 | AX159517 Sequence |
| 12 | 12.6 | 54.8 | 27 | 6 | AX126102 | AX126102 Sequence |
| 13 | 12.6 | 54.8 | 27 | 6 | AX117880 | AX117880 Sequence |
| 14 | 12.6 | 54.8 | 39 | 6 | AR069156 | AR069156 Sequence |
| 15 | 12.6 | 54.8 | 39 | 6 | I49577 | I49577 Sequence 26 |
| 16 | 12.6 | 54.8 | 51 | 6 | AX158897 | AX158897 Sequence |
| 17 | 12.6 | 54.8 | 51 | 6 | AX158898 | AX158898 Sequence |
| 18 | 12.4 | 53.9 | 26 | 6 | AX003626 | AX003626 Sequence |
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| 20 | 12.4 | 53.9 | 44 | 10 | RATM/C134 | R02426 Rat fast my |
| 21 | 12.4 | 53.9 | 46 | 6 | A16157 | A16157 primer. 10/ |
| 22 | 12.4 | 53.9 | 51 | 6 | AX116281 | AX116281 Sequence |
| 23 | 12.4 | 53.9 | 51 | 10 | AF005618 | AF005618 Mus muscu |
| 24 | 12.4 | 53.9 | 56 | 9 | S77443 | S77443 Ig VH-immun |
| 25 | 12.2 | 53.0 | 40 | 6 | AR053641 | AR053641 Sequence |
| 26 | 12.2 | 53.0 | 40 | 6 | AR053647 | AR053647 Sequence |
| 27 | 12.2 | 53.0 | 44 | 6 | AX034957 | AX034957 Sequence |
| 28 | 12.2 | 53.0 | 45 | 6 | AR139753 | AR139753 Sequence |
| 29 | 12.2 | 52.2 | 20 | 6 | AR100167 | AR100167 Sequence |
| 30 | 12 | 52.2 | 20 | 6 | AR137857 | AR137857 Sequence |
| 31 | 12 | 52.2 | 20 | 6 | AR149851 | AR149851 Sequence |
| 32 | 12 | 52.2 | 20 | 6 | I77253 | I77253 Sequence 17 |
| 33 | 12 | 52.2 | 26 | 6 | AR125844 | AR125844 Sequence |
| 34 | 12 | 52.2 | 26 | 6 | AR126103 | AR126103 Sequence |
| 35 | 12 | 52.2 | 26 | 6 | AR140988 | AR140988 Sequence |
| 36 | 12 | 52.2 | 26 | 6 | I47256 | I47256 Sequence 18 |
| 37 | 12 | 52.2 | 30 | 6 | AR125766 | AR125766 Sequence |
| 38 | 12 | 52.2 | 30 | 6 | E27394 | E27394 Process for |
| 39 | 12 | 52.2 | 30 | 6 | I47178 | I47178 Sequence 10 |
| 40 | 12 | 52.2 | 31 | 6 | A17338 | A17338 partial int |
| 41 | 12 | 52.2 | 35 | 6 | AR140989 | AR140989 Sequence |
| 42 | 12 | 52.2 | 37 | 6 | I34928 | I34928 Sequence 14 |
| 43 | 12 | 52.2 | 39 | 6 | E11361 | E11361 DNA encodin |
| 44 | 12 | 52.2 | 40 | 6 | I86249 | I86249 Sequence 3 |
| 45 | 12 | 52.2 | 45 | 6 | A28989 | A28989 oligo 8 fro |

ALIGNMENTS

RESULT 1
AX159518
LOCUS AX159518 51 bp DNA
DEFINITION Sequence 2846 from Patent WO0140521.
ACCESSION AX159518
VERSION AX159518.1 GI:14540849
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 51)
Shinketsu, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0140521-A 2846 07-JUN-2001;
Curagen Corporation (US)
Location/Qualifiers
1..51
/organism="Homo sapiens"

FEATURES
source

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misc-feature 26 /db_xref="taxon:9606"
      /note="2 of 2 allelic variants (2845 is other entry)
Accession number c942527623"
BASE COUNT 13 a 17 c 16 g 5 t
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Query Match 61.7%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gaacaccgcctctcgca 21
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Db 9 GAACACCAGGCTCTCACA 27

RESULT 2
LOCUS AR026622 30 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5856121.
ACCESSION AR026622
VERSION AR026622.1 GI:5937462
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Gorski,D.H. and Walsh,K.
TITLE Growth arrest homebox gene
JOURNAL Patent: US 5856121-A 14 05-JAN-1999;
FEATURES
    SOURCE 1..30
    ORIGIN /organism="Unknown"
BASE COUNT 4 a 13 c 8 g 5 t
ORIGIN

Query Match 57.4%; Score 13.2; DB 6; Length 30;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gaacaccgcctctcgcg 20
   ||||| ||||| ||
Db 13 GAACACCCCTCTTTGGC 30

RESULT 3
LOCUS S59766 36 bp mRNA PRI 20-MAR-2000
DEFINITION IGHV-pre-B-specific immunoglobulin heavy chain variable region
(CDR3 region, V-D-J rearrangement, clone LE 1-17) [human, bone
marrow, mRNA Recombinant Partial, 36 nt].
ACCESSION S59766
VERSION S59766
KEYWORDS S59766.1 GI:385405
SOURCE human bone marrow.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS Millil,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
Fougerneau,M. and Schiff,C.
TITLE Bone marrow cells in X-linked agammaglobulinemia express
pre-B-specific genes (lambda-like and V pre-B) and present
immunoglobulin V-D-J gene usage strongly biased to a fetal-like
reertoire
J. Clin. Invest. 91 (4), 1616-1629 (1993)
93232287
JOURNAL GenBank Staff at the National Library of Medicine created this
entry [NCBI gidsq 131828] from the original journal article.
REMARK This sequence comes from Fig. 3.
Map location: X.

FEATURES
    source Location/Qualifiers
    gene 1..36
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /partial
      /gene="IGHV"
      /note="pre-B-specific immunoglobulin heavy chain variable
region"
BASE COUNT 6 a 3 c 15 g 12 t
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Query Match 57.4%; Score 13.2; DB 9; Length 36;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 caccgcctctcgcaaa 23
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Db 18 CAACCCCTCTCTGCACA 1

RESULT 4
LOCUS AX007196 34 bp DNA PAT 06-SEP-2000
DEFINITION Sequence 36 from Patent WO0000618.
ACCESSION AX007196
VERSION AX007196.1 GI:9995062
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 34)
AUTHORS Leadlay,P.F., Cortes,J., Staunton,J. and Mcarthur,H.A.
TITLE Polyketides and their synthesis
JOURNAL Patent: WO 0000618-A 36 06-JAN-2000;
LEADLAY PETER FRANCIS (GB); CORTES JESUS (GB); STAUNTON JAMES (GB);
BIOTICA TECH LTD (GB); MCARTHUR HAMISH ALASTAIR IRVIN (US)
FEATURES
    source 1..34
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="Oligonucleotide"
BASE COUNT 7 a 10 c 8 g 9 t
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 34;
Best Local Similarity 76.2%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 gagaacaccgcctctcgca 21
   ||||| || || || ||
Db 12 GAGACTCGCGATTTCGCCCA 32

RESULT 5
LOCUS AX007368 34 bp DNA PAT 06-SEP-2000
DEFINITION Sequence 36 from Patent WO0000500.
ACCESSION AX007368
VERSION AX007368.1 GI:9995138
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 34)
AUTHORS Leadlay,P.F., Cortes,J., Staunton,J. and Mcarthur,H.A.
TITLE Polyketides and their synthesis
JOURNAL Patent: WO 0000500-A 36 06-JAN-2000;
LEADLAY PETER FRANCIS (GB); CORTES JESUS (GB); STAUNTON JAMES (GB);
BIOTICA TECH LTD (GB); PFIZER (US); MCARTHUR HAMISH ALASTAIR IRVIN
(US)
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FEATURES
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/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 7 a 10 c 8 g 9 t
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 34;
Best Local Similarity 76.2%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 gagaacaccgcgtctcgcga 21
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Db 12 GAGAACTCGCGATTTCGCCGA 32

RESULT 6
AX160002 51 bp DNA PAT 22-JUN-2001
LOCUS AX160002 Sequence 3330 from Patent WO0140521.
DEFINITION AX160002
ACCESSION AX160002
VERSION AX160002.1 GI:14541333
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acid containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0140521-A 3330 07-JUN-2001;
JOURNAL Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc.feature
/note="2 of 2 allelic variants (3329 is other entry)
Accession number cg43247175"

BASE COUNT 15 a 13 c 14 g 9 t
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 51;
Best Local Similarity 76.2%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 gagaacaccgcgtctcgcga 21
||||| ||| ||| ||| ||| |||
Db 6 GAGAGGCCAGCTTCTCCCA 26

RESULT 7
POBBS5E 52 bp mRNA PHG 28-APR-1993
LOCUS POBBS5E Bacteriophage Q-beta minus strand RNA, 5' terminus.
DEFINITION Bacteriophage Q-beta minus strand RNA, 5' terminus.
ACCESSION M57754
VERSION M57754.1 GI:215716
KEYWORDS
SOURCE Bacteriophage Q-beta RNA.
ORGANISM Bacteriophage Q-beta
Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
Allolevivirus; Allolevivirus subgroup III.
REFERENCE 1 (bases 1 to 52)
AUTHORS Goodman, H.M., Biller, M.A., Hindley, J. and Weissmann, C.
TITLE The nucleotide sequence at the 5'-terminus of the Q-beta RNA minus
strand
Proc. Natl. Acad. Sci. U.S.A. 67, 921-928 (1970)
JOURNAL From EMBL 27 entry POBBS5E; dated 13-FEB-1991.
COMMENT Location/Qualifiers
FEATURES

source 1..52
/organism="Bacteriophage Q-beta"
/db_xref="taxon:12009"

BASE COUNT 15 a 11 c 17 g 9 t
ORIGIN

Query Match 56.5%; Score 13; DB 7; Length 52;
Best Local Similarity 76.2%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaacaccgcgtctcgcga 22
||| ||| ||| ||| ||| |||
Db 32 AGATCCCCCTCTCACTCGTAA 12

RESULT 8
POBPS3E 52 bp ss-RNA PHG 28-APR-1993
LOCUS POBPS3E/B C Bacteriophage Q-beta plus-strand RNA, 3' terminus.
DEFINITION Bacteriophage Q-beta plus-strand RNA, 3' terminus.
ACCESSION M25462
VERSION M25462.1 GI:215723
KEYWORDS
SOURCE Bacteriophage Q-beta RNA.
ORGANISM Bacteriophage Q-beta
Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
Allolevivirus; Allolevivirus subgroup III.
REFERENCE 1 (bases 1 to 52)
AUTHORS Goodman, H.M., Biller, M.A., Hindley, J. and Weissmann, C.
TITLE The nucleotide sequence at the 5'-terminus of the Q-beta RNA minus
strand
Proc. Natl. Acad. Sci. U.S.A. 67, 921-928 (1970)
JOURNAL Location/Qualifiers
FEATURES source 1..52
/organism="Bacteriophage Q-beta"
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BASE COUNT 9 a 17 c 11 g 15 t
ORIGIN

Query Match 56.5%; Score 13; DB 7; Length 52;
Best Local Similarity 76.2%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaacaccgcgtctcgcga 22
||| ||| ||| ||| ||| |||
Db 32 AGATCCCCCTCTCACTCGTAA 12

RESULT 9
A93667/C 41 bp DNA PAT 22-JAN-2000
LOCUS A93667 Sequence 3 from Patent WO9734144.
DEFINITION A93667
ACCESSION A93667
VERSION A93667.1 GI:6741855
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 41)
AUTHORS Langer, G. and Troschl, L.
TITLE METHOD OF DETECTING THE EFFECT OF TEST SUBSTANCES USING HEN
UROKINASE
Patent: WO 9734144-A 3 18-SEP-1997;
JOURNAL SCHERING AG (DE); LANGER GERNOT (DE)
FEATURES Location/Qualifiers
source 1..41
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 5 a 14 c 15 g 7 t
ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 41;
Best Local Similarity 87.5%; Pred. No. 3.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 aacacccgctctcgc 19
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Db 33 ACCACCCGCTTCTCG 18

RESULT 10
AX158612 50 bp DNA PAT 22-JUN-2001
LOCUS AX158612/c
DEFINITION Sequence 1940 from Patent WO0140521.
ACCESSION AX158612
VERSION AX158612.1 GI:14539943
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 1940 07-JUN-2001;
CURAGEN Corporation (US)
FEATURES
LOCATION/Qualifiers
1..50
misc_feature
/organism="Homo sapiens"
/db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number C938034239"

BASE COUNT 11 a 13 c 18 g 8 t
ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gagaacccgctctc 16
| | | | | | | | | |
Db 28 GAGTACCGCCGCTCTC 13

RESULT 11
AX159517 51 bp DNA PAT 22-JUN-2001
LOCUS AX159517
DEFINITION Sequence 2845 from Patent WO0140521.
ACCESSION AX159517
VERSION AX159517.1 GI:14540848
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2845 07-JUN-2001;
CURAGEN Corporation (US)
FEATURES
LOCATION/Qualifiers
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26
/note="1 of 2 allelic variants (2846 is other entry)
Accession number C942527623"

BASE COUNT 13 a 16 c 17 g 5 t

ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred. No. 3.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 gaacacccgctctc 18
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Db 9 GAACACCGCTCTCTC 24

RESULT 12
AR126102 27 bp DNA PAT 16-MAY-2001
LOCUS AR126102/c
DEFINITION Sequence 444 from patent US 6177557.
ACCESSION AR126102
VERSION AR126102.1 GI:14112164
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Janjic, N., Gold, L. and Tasset, D.
TITLE High affinity ligands of basic fibroblast growth factor and thrombin
JOURNAL Patent: US 6177557-A 444 23-JAN-2001;
CURAGEN Corporation (US)
FEATURES
LOCATION/Qualifiers
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misc_feature
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/db_xref="taxon:9606"
4 a 3 c 13 g 6 t 1 others

BASE COUNT 4 a 3 c 13 g 6 t 1 others
ORIGIN

Query Match 54.8%; Score 12.6; DB 6; Length 27;
Best Local Similarity 69.6%; Pred. No. 4.6e+04;
Matches 16; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 gagaacccgctctcga 23
| | | | | | | | | |
Db 27 GAAACACCGCTCTCTCACA 5

RESULT 13
AX117880 27 bp DNA PAT 11-MAY-2001
LOCUS AX117880/c
DEFINITION Sequence 3003 from Patent WO0129262.
ACCESSION AX117880
VERSION AX117880.1 GI:14034831
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Picoult-Newbury, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3003 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
LOCATION/Qualifiers
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misc_feature
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
1..27
/note="n = C3 linker"

BASE COUNT 4 a 5 c 11 g 6 t 1 others
ORIGIN

Query Match 54.8%; Score 12.6; DB 6; Length 27;
Best Local Similarity 75.0%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaaccgcgtctcgcga 21
| | | | |
Db 23 ACANCAACCGCATCTCGCA 4

RESULT 14
AR069156 AR069156 39 bp DNA PAT 18-FEB-2000
LOCUS Sequence 26 from patent US 5891442.
ACCESSION AR069156
VERSION AR069156.1 GI:7220044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 39)
AUTHORS Paolletti, E., Taylor, J. and Gettig, R.
TITLE Infectious bursal disease virus recombination poxvirus vaccine
JOURNAL Patent: US 5891442-A 26 06-APR-1999;
FEATURES Location/Qualifiers
source 1..39
BASE COUNT 10 a 12 c 10 g 7 t
ORIGIN

Query Match 54.88; Score 12.6; DB 6; Length 39;
Best Local Similarity 78.98; Pred. No. 4.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 aaccaccgcgtctcgcga 22
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Db 3 AACACGAGCTCTCCCCCA 21

RESULT 15
149577 149577 39 bp DNA PAT 07-OCT-1997
LOCUS Sequence 26 from patent US 5641490.
ACCESSION 149577
VERSION 149577.1 GI:2471797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 39)
AUTHORS Paolletti, E., Taylor, J. and Gettig, R.
TITLE Infectious bursal disease virus recombinant poxvirus vaccine
JOURNAL Patent: US 5641490-A 26 24-JUN-1997;
FEATURES Location/Qualifiers
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BASE COUNT 10 a 12 c 10 g 7 t
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OY 4 aaccaccgcgtctcgcga 22
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Job time: 11122 sec

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